OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/826,752

DATE: 04/30/2001
TIME: 11:04:49

Input Set : A:\0050.1491-005.TXT
Output Set: N:\CRF3\04302001\I826752.raw

ENTERED

```
  4 <110> APPLICANT: Guarente, Leonard P.
  5        Austriaco Jr., Nicanor
  6        Claus, James J.
  7        Cole, Francesca
  8        Kennedy, Brian
 11 <120> TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
 12        YEAST
 14 <130> FILE REFERENCE: 0050.1491-005
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/826,752
C--> 16 <141> CURRENT FILING DATE: 2001-04-05
 16 <150> PRIOR APPLICATION NUMBER: US 08/396,001
 17 <151> PRIOR FILING DATE: 1995-02-28
 19 <150> PRIOR APPLICATION NUMBER: PCT/US94/09351
 20 <151> PRIOR FILING DATE: 1994-08-15
 22 <150> PRIOR APPLICATION NUMBER: US 08/107,408
 23 <151> PRIOR FILING DATE: 1993-08-16
 25 <150> PRIOR APPLICATION NUMBER: US 09/323,433
 26 <151> PRIOR FILING DATE: 1999-06-01
 28 <160> NUMBER OF SEQ ID NOS: 48
 30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 1946
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Saccharomyces cerevisiae
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (322)...(1671)
 40 <223> OTHER INFORMATION: UTH1
 42 <400> SEQUENCE: 1
 43 tgaaaaagtg gaactagacc ccacgtcagc gggcctaggc ccttcaatgt gttagaatac 60
 44 acagcgtgcc tagttcctgg tgcctggatc tcgaggccgc ggcactggaa aagccctttc 120
 45 ttttccagat cgggaaacct aatgagtcca taaaaagaaa tgtagaggtg gtgttgacgt 180
 46 tttgccgctt ttgggcaagt aggtctttct gcacggcccg gcccgggtcg tgcggaaaaa 240
 47 gaaaaaagca gacaaaacaa aatttttcct ttttttcgcc tttgtttctc ctgattcggg 300
 48 tatataagtg aataccatct a atg tgt ttc ctt ctc gag acc tcg gcg tct   351
 49                          Met Cys Phe Leu Leu Glu Thr Ser Ala Ser
 50                           1               5                  10
 52 ccc aga tca aag ctc agc aaa gat ttt aaa ccg caa ttt acg ctc ctt   399
 53 Pro Arg Ser Lys Leu Ser Lys Asp Phe Lys Pro Gln Phe Thr Leu Leu
 54                 15                  20                  25
 56 tca tcg gta act aag aag aaa aaa aaa aaa gta cga cca cac aat ttc   447
 57 Ser Ser Val Thr Lys Lys Lys Lys Lys Lys Val Arg Pro His Asn Phe
 58             30                  35                  40
 60 cag tgt att cat tcc tta aac ttc gtt tat ttt tta ttc att cat tca   495
 61 Gln Cys Ile His Ser Leu Asn Phe Val Tyr Phe Leu Phe Ile His Ser
 62         45                  50                  55
 64 ttt tta ttt gaa tat aac caa cta cta gtc ctt cct tta aac aaa aat   543
```

```
 65 Phe Leu Phe Glu Tyr Asn Gln Leu Leu Val Leu Pro Leu Asn Lys Asn
 66      60              65              70
 68 tta ccc tcc ctt aat ttt tca aga aat tcc agt atg aaa tta tcc gct    591
 69 Leu Pro Ser Leu Asn Phe Ser Arg Asn Ser Ser Met Lys Leu Ser Ala
 70  75              80              85              90
 72 cta tta gct tta tca gcc tcc acc gcc gtc ttg gcc gct cca gct gtc    639
 73 Leu Leu Ala Leu Ser Ala Ser Thr Ala Val Leu Ala Ala Pro Ala Val
 74              95              100             105
 76 cac cat agt gac aac cac cac cac aac gac aag cgt gcc gtt gtc acc    687
 77 His His Ser Asp Asn His His His Asn Asp Lys Arg Ala Val Val Thr
 78          110             115             120
 80 gtt act cag tac gtc aac gca gac ggc gct gtt gtt att cca gct gcc    735
 81 Val Thr Gln Tyr Val Asn Ala Asp Gly Ala Val Val Ile Pro Ala Ala
 82          125             130             135
 84 acc acc gct acc tcg gcg gct gct gat gga aag gtc gag tct gtt gct    783
 85 Thr Thr Ala Thr Ser Ala Ala Ala Asp Gly Lys Val Glu Ser Val Ala
 86      140             145             150
 88 gct gcc acc act act ttg tcc tcg act gcc gcc gcc gct act acc tct    831
 89 Ala Ala Thr Thr Thr Leu Ser Ser Thr Ala Ala Ala Thr Thr Ser
 90 155             160             165             170
 92 gcc gcc gcc tct tct tcc tcc tct tcc tct tcc tcc tct tcc tct tct    879
 93 Ala Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 94              175             180             185
 96 tcc tct gtt ggt tct gga gat ttt gaa gat ggt acc att tcc tgt tct    927
 97 Ser Ser Val Gly Ser Gly Asp Phe Glu Asp Gly Thr Ile Ser Cys Ser
 98              190             195             200
100 gat ttc cca tcc gga caa ggt gct gtc tcc ttg gac tgg tta ggt cta    975
101 Asp Phe Pro Ser Gly Gln Gly Ala Val Ser Leu Asp Trp Leu Gly Leu
102          205             210             215
104 ggc ggc tgg gct tcc atc atg gac atg aac ggt aac acc gcc acc tct   1023
105 Gly Gly Trp Ala Ser Ile Met Asp Met Asn Gly Asn Thr Ala Thr Ser
106      220             225             230
108 tgt caa gac gga tac tac tgt tct tac gct tgt tct cca ggt tac gct   1071
109 Cys Gln Asp Gly Tyr Tyr Cys Ser Tyr Ala Cys Ser Pro Gly Tyr Ala
110 235             240             245             250
112 aag acc caa tgg cct tct gaa caa cct tcc gat ggt aga tcc gtt ggt   1119
113 Lys Thr Gln Trp Pro Ser Glu Gln Pro Ser Asp Gly Arg Ser Val Gly
114              255             260             265
116 ggt tta tac tgt aag aac ggt aaa tta tac cgt tcc aac acc gac act   1167
117 Gly Leu Tyr Cys Lys Asn Gly Lys Leu Tyr Arg Ser Asn Thr Asp Thr
118              270             275             280
120 aac agt ttg tgt gta gaa ggt caa ggc tct gct caa gct gtt aac aag   1215
121 Asn Ser Leu Cys Val Glu Gly Gln Gly Ser Ala Gln Ala Val Asn Lys
122          285             290             295
124 gtc tcc ggc tcc att gct atc tgt ggt acc gat tat cca ggt tct gaa   1263
125 Val Ser Gly Ser Ile Ala Ile Cys Gly Thr Asp Tyr Pro Gly Ser Glu
126      300             305             310
128 aac atg gtc gtt cct acc gta gtt ggc gct ggt tcc tcc caa cca atc   1311
129 Asn Met Val Val Pro Thr Val Val Gly Ala Gly Ser Ser Gln Pro Ile
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Input Set : A:\0050.1491-005.TXT
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130 315                   320              325              330
132 aac gtc atc aag gag gac tcc tac tat caa tgg caa ggt aag aag acc   1359
133 Asn Val Ile Lys Glu Asp Ser Tyr Tyr Gln Trp Gln Gly Lys Lys Thr
134               335              340              345
136 tct gcc caa tac tac gtt aac aac gct ggt gtc tct gtg gaa gat ggt   1407
137 Ser Ala Gln Tyr Tyr Val Asn Asn Ala Gly Val Ser Val Glu Asp Gly
138               350              355              360
140 tgt atc tgg ggt act gag ggt tcc ggt gtc ggt aac tgg gcc cca gtt   1455
141 Cys Ile Trp Gly Thr Glu Gly Ser Gly Val Gly Asn Trp Ala Pro Val
142          365              370              375
144 gtc ttg ggt gct ggt tac act gat ggt atc act tac ttg tcc atc att   1503
145 Val Leu Gly Ala Gly Tyr Thr Asp Gly Ile Thr Tyr Leu Ser Ile Ile
146     380              385              390
148 cca aac cca aac aac aaa gaa gca cca aac ttt aac atc aag atc gtt   1551
149 Pro Asn Pro Asn Asn Lys Glu Ala Pro Asn Phe Asn Ile Lys Ile Val
150 395              400              405              410
152 gcc acc gat ggc tct acc gtc aat ggt gct tgc tct tac gaa aat ggt   1599
153 Ala Thr Asp Gly Ser Thr Val Asn Gly Ala Cys Ser Tyr Glu Asn Gly
154               415              420              425
156 gtc tac tct ggc tct ggc tct gac ggt tgt act gtt tca gtt act tct   1647
157 Val Tyr Ser Gly Ser Gly Ser Asp Gly Cys Thr Val Ser Val Thr Ser
158          430              435              440
160 ggt tct gct aac ttt gtc ttc tac taggcctttt ttccttgaat attgcaaata   1701
161 Gly Ser Ala Asn Phe Val Phe Tyr
162          445              450
164 agcttttgct agtacttttt ttactccgtt catttttatgg tttatttttc aattagttcg   1761
165 tttttccaca atacaaaaaa acacagtcct ttgtactatc cctttatttt cattattttt   1821
166 tcttttttaa gataccacta gatattatca tatatagcat attatataac ataaaaagtc   1881
167 aagaaaaaaa atgtttttat cactttctat aactgcatat cttttttttgc atttcgaatg   1941
                                                                        1946
168 attgc
170 <210> SEQ ID NO: 2
171 <211> LENGTH: 450
172 <212> TYPE: PRT
173 <213> ORGANISM: Saccharomyces cerevisiae
175 <220> FEATURE:
176 <221> NAME/KEY: VARIANT
177 <222> LOCATION: (1)...(441)
178 <223> OTHER INFORMATION: Xaa = Any Amino Acid
180 <400> SEQUENCE: 2
181 Met Cys Phe Leu Leu Glu Thr Ser Ala Ser Pro Arg Ser Lys Leu Ser
182 1               5               10              15
183 Lys Asp Phe Lys Pro Gln Phe Thr Leu Leu Ser Ser Val Thr Lys Lys
184          20              25              30
185 Lys Lys Lys Lys Val Arg Pro His Asn Phe Gln Cys Ile His Ser Leu
186     35              40              45
187 Asn Phe Val Tyr Phe Leu Phe Ile His Ser Phe Leu Phe Glu Tyr Asn
188     50              55              60
189 Gln Leu Leu Val Leu Pro Leu Asn Lys Asn Leu Pro Ser Leu Asn Phe
190 65              70              75              80
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Input Set : A:\0050.1491-005.TXT
Output Set: N:\CRF3\04302001\I826752.raw

```
191 Ser Arg Asn Ser Ser Met Lys Leu Ser Ala Leu Leu Ala Leu Ser Ala
192                 85              90              95
193 Ser Thr Ala Val Leu Ala Ala Pro Ala Val His His Ser Asp Asn His
194             100             105             110
195 His His Asn Asp Lys Arg Ala Val Val Thr Val Thr Gln Tyr Val Asn
196         115             120             125
197 Ala Asp Gly Ala Val Val Ile Pro Ala Ala Thr Thr Ala Thr Ser Ala
198     130             135             140
199 Ala Ala Asp Gly Lys Val Glu Ser Val Ala Ala Ala Thr Thr Thr Leu
200 145             150             155             160
201 Ser Ser Thr Ala Ala Ala Ala Thr Thr Ser Ala Ala Ala Ser Ser Ser
202             165             170             175
203 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Val Gly Ser Gly
204             180             185             190
205 Asp Phe Glu Asp Gly Thr Ile Ser Cys Ser Asp Phe Pro Ser Gly Gln
206         195             200             205
207 Gly Ala Val Ser Leu Asp Trp Leu Gly Leu Gly Trp Ala Ser Ile
208     210             215             220
209 Met Asp Met Asn Gly Asn Thr Ala Thr Ser Cys Gln Asp Gly Tyr Tyr
210 225             230             235             240
211 Cys Ser Tyr Ala Cys Ser Pro Gly Tyr Ala Lys Thr Gln Trp Pro Ser
212             245             250             255
213 Glu Gln Pro Ser Asp Gly Arg Ser Val Gly Gly Leu Tyr Cys Lys Asn
214         260             265             270
215 Gly Lys Leu Tyr Arg Ser Asn Thr Asp Thr Asn Ser Leu Cys Val Glu
216         275             280             285
217 Gly Gln Gly Ser Ala Gln Ala Val Asn Lys Val Ser Gly Ser Ile Ala
218     290             295             300
219 Ile Cys Gly Thr Asp Tyr Pro Gly Ser Glu Asn Met Val Val Pro Thr
220 305             310             315             320
221 Val Val Gly Ala Gly Ser Ser Gln Pro Ile Asn Val Ile Lys Glu Asp
222             325             330             335
223 Ser Tyr Tyr Gln Trp Gln Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Val
224             340             345             350
225 Asn Asn Ala Gly Val Ser Val Glu Asp Gly Cys Ile Trp Gly Thr Glu
226         355             360             365
227 Gly Ser Gly Val Gly Asn Trp Ala Pro Val Val Leu Gly Ala Gly Tyr
228     370             375             380
229 Thr Asp Gly Ile Thr Tyr Leu Ser Ile Ile Pro Asn Pro Asn Asn Lys
230 385             390             395             400
231 Glu Ala Pro Asn Phe Asn Ile Lys Ile Val Ala Thr Asp Gly Ser Thr
232             405             410             415
233 Val Asn Gly Ala Cys Ser Tyr Glu Asn Gly Val Tyr Ser Gly Ser Gly
234             420             425             430
235 Ser Asp Gly Cys Thr Val Ser Val Thr Ser Gly Ser Ala Asn Phe Val
236         435             440             445
237 Phe Tyr
238     450
241 <210> SEQ ID NO: 3
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242 <211> LENGTH: 3455
243 <212> TYPE: DNA
244 <213> ORGANISM: Saccharomyces cerevisiae
246 <220> FEATURE:
247 <221> NAME/KEY: CDS
248 <222> LOCATION: (663)...(3164)
249 <223> OTHER INFORMATION: UTH4
251 <400> SEQUENCE: 3
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253 gatcagccta tcgacacgcc ttttttagcg gtctaacaat ctccgtttat gtcgtatgga 120
254 atttctatac ttgaccctac cttatttctc gaatatgcct ataaggattt tctcgaaaga 180
255 agggcttcgg gaaagaggcg cctcaggcaa aaatgagcaa aaaaaaaaa aaaaagaaaa 240
256 gattcgaaga tctatgaaaa atttatgcag attcgttgag agttataagg attttactct 300
257 ttatggttat aggtttcatt ctaaaatcaa gcataaattt tgtgttttgt cttcctcttt 360
258 tcctgtcctc ttttttgcc atcctctgtc gccattgaag tcgaacttta tagatagatt 420
259 tactcttgat tctcacgcat ctcaggccac ctggacactg tacatggttg tgattgttct 480
260 ctttctcagt tatcgaaatt gatcctaggc ttatactcca aaatcggctc tgcacacgcc 540
261 ttatttttgt ggtttcactt tactaacaca acattctttt attcaatcag atcaataacg 600
262 aaccatttcc atctgccgac tcagcatcga ttttaactac gtctacatca aataactcct 660
263 ta atg tct tac aat cat cag cct caa cta tct att aac tcc gtc caa     707
264    Met Ser Tyr Asn His Gln Pro Gln Leu Ser Ile Asn Ser Val Gln
265    1               5                   10                  15
267 tca ctc ttg gag ccc gtg acc cct ccg cct ttg ggc cag atg aat aac   755
268 Ser Leu Leu Glu Pro Val Thr Pro Pro Pro Leu Gly Gln Met Asn Asn
269             20                  25                  30
271 aaa aga aac cat caa aag gct cat tcg ctt gat ctc tct ggt ttt aat   803
272 Lys Arg Asn His Gln Lys Ala His Ser Leu Asp Leu Ser Gly Phe Asn
273             35                  40                  45
275 cag ttc ata tca tcg aca caa tct ccc ttg gct ttg atg aat aat aca   851
276 Gln Phe Ile Ser Ser Thr Gln Ser Pro Leu Ala Leu Met Asn Asn Thr
277         50                  55                  60
279 tca aca tcg aat tct gct aac tct ttt tcc ccg aat cct aat gct gct   899
280 Ser Thr Ser Asn Ser Ala Asn Ser Phe Ser Pro Asn Pro Asn Ala Ala
281     65                  70                  75
283 agc aac tcc act ggg ctt tca gcc tca atg gca aat cct cca gcc att   947
284 Ser Asn Ser Thr Gly Leu Ser Ala Ser Met Ala Asn Pro Pro Ala Ile
285 80                  85                  90                  95
287 cta cca tta atc aat gag ttt gat ctg gaa atg gat ggt ccc agg aga   995
288 Leu Pro Leu Ile Asn Glu Phe Asp Leu Glu Met Asp Gly Pro Arg Arg
289             100                 105                 110
291 aaa tca agc cac gat ttc acg gtt gtt gct cct tcg aac tct ggt gtc   1043
292 Lys Ser Ser His Asp Phe Thr Val Val Ala Pro Ser Asn Ser Gly Val
293         115                 120                 125
295 aat acc tcc agt tta att atg gaa aca cca tcc tct tca gtg act cct   1091
296 Asn Thr Ser Ser Leu Ile Met Glu Thr Pro Ser Ser Ser Val Thr Pro
297         130                 135                 140
299 gct gca tct ctc aga aat ttt agc aat agt aat aat gct gct tcc aaa   1139
300 Ala Ala Ser Leu Arg Asn Phe Ser Asn Ser Asn Asn Ala Ala Ser Lys
301     145                 150                 155
```

_fyi_

**Please Not :**  
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequenc Listing to ensure that a corresp nding explanation is presented in the <220> to <223> fields of each sequence which pres nts at least one n r Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION:   US/09/826,752

DATE: 04/30/2001
TIME: 11:04:50

Input Set : A:\0050.1491-005.TXT
Output Set: N:\CRF3\04302001\I826752.raw

```
L:16   M:270 C: Current Application Number differs, Replaced Current Application No
L:16   M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
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